

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 29, 2004, 14:59:54 ; Search time 3 seconds
(without alignments)
4.215 Million cell updates/sec

Title: SEQ809
Perfect score: 798
Sequence: 1 MEIIKKFVALGLLSAVLSSS.....VYAPNKIQLDMVSGVGSIC 148

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 497 seqs, 85440 residues
Total number of hits satisfying chosen parameters: 497

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : US08487032A.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	775	97.1	170	US-08-487-032A-764	Sequence 764, App
2	125.5	15.7	80	US-08-487-032A-808	Sequence 808, App
3	93.5	11.7	157	US-08-487-032A-403	Sequence 403, App
4	67.5	8.5	325	US-08-487-032A-833	Sequence 833, App
5	64	8.0	264	US-08-487-032A-498	Sequence 498, App
6	55.5	7.0	560	US-08-487-032A-708	Sequence 708, App
7	52.5	6.6	343	US-08-487-032A-632	Sequence 632, App
8	49	6.1	127	US-08-487-032A-595	Sequence 595, App
9	49	6.1	155	US-08-487-032A-777	Sequence 777, App
10	49	6.1	1178	US-08-487-032A-473	Sequence 473, App
11	46	5.8	214	US-08-487-032A-663	Sequence 663, App
12	46	5.8	325	US-08-487-032A-671	Sequence 671, App
13	44.5	5.6	199	US-08-487-032A-651	Sequence 651, App
14	44.5	5.6	237	US-08-487-032A-482	Sequence 482, App
15	44	5.5	308	US-08-487-032A-573	Sequence 573, App
16	44	5.5	421	US-08-487-032A-479	Sequence 479, App
17	43.5	5.5	351	US-08-487-032A-639	Sequence 639, App
18	43	5.4	210	US-08-487-032A-725	Sequence 725, App
19	42.5	5.3	496	US-08-487-032A-629	Sequence 629, App
20	42.5	5.3	187	US-08-487-032A-445	Sequence 445, App
21	42.5	5.3	237	US-08-487-032A-635	Sequence 635, App
22	42	5.3	164	US-08-487-032A-817	Sequence 817, App
23	42	5.3	422	US-08-487-032A-548	Sequence 548, App
24	41.5	5.2	509	US-08-487-032A-384	Sequence 384, App
25	41	5.1	121	US-08-487-032A-698	Sequence 698, App
26	41	5.1	162	US-08-487-032A-612	Sequence 612, App
27	41	5.1	702	US-08-487-032A-585	Sequence 585, App
28	40.5	5.1	240	US-08-487-032A-854	Sequence 854, App
29	40	5.0	133	US-08-487-032A-386	Sequence 386, App
30	40	5.0	179	US-08-487-032A-853	Sequence 853, App
31	40	5.0	200	US-08-487-032A-751	Sequence 751, App
32	40	5.0	313	US-08-487-032A-535	Sequence 535, App
33	39.5	4.9	198	US-08-487-032A-626	Sequence 626, App

34	39.5	4.9	231	1	US-08-487-032A-560	Sequence 560, App
35	39.5	4.9	233	1	US-08-487-032A-503	Sequence 503, App
36	39.5	4.9	309	1	US-08-487-032A-816	Sequence 816, App
37	39.5	4.9	339	1	US-08-487-032A-574	Sequence 574, App
38	39	4.9	173	1	US-08-487-032A-786	Sequence 786, App
39	39	4.9	193	1	US-08-487-032A-413	Sequence 413, App
40	39	4.9	193	1	US-08-487-032A-571	Sequence 571, App
41	39	4.9	278	1	US-08-487-032A-404	Sequence 404, App
42	39	4.9	286	1	US-08-487-032A-703	Sequence 703, App
43	39	4.9	341	1	US-08-487-032A-601	Sequence 601, App
44	38.5	4.8	213	1	US-08-487-032A-490	Sequence 490, App
45	38.5	4.8	237	1	US-08-487-032A-519	Sequence 519, App

ALIGNMENTS

Query Match	97.1% ; Score 775 ; DB 1 ; Length 170 ;
Best Local Similarity	98.6% ; Pred. No. 3.4e-70 ;
Matches 144 ;	Conservative 0 ; Mismatches 2 ; Indels 0 ; Gaps 0 ;
QY	8080
DB	1
QY	61
DB	61
QY	121
DB	121

RESULT 7
US-08-487-032A-632

ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
US-08-487-032A-777

Query Match 6.1%; Score 49; DB 1; Length 155;
Best Local Similarity 20.3%; Pred. No. 3;
Matches 16; Conservative 10; Mismatches 17; Indels 36; Gaps 3;

QY 101 KSLDNTSKR-----FGFRVYGLPDYGHAD-----LGRQ--- 128
DB 14 RSKALTRSGINFSKNTLVAFMGPFDYAHANSIKLKNPNYNSBAQVASQILGRQFIN 73
QY 129 ----VYAPNKIQLDMWSWG 143
DB 74 RLNTIADPTREPPNMLTYG 92

RESULT 10
US-08-487-032A-473
Sequence 473, Application US/08487032A
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 880
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,032A
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 473:
SEQUENCE CHARACTERISTICS:
LENGTH: 1178 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1...1178
OTHER INFORMATION: /note="cytotoxicity associated immunodominant antigen [H.
US-08-487-032A-473

Query Match 6.1%; Score 49; DB 1; Length 1178;
Best Local Similarity 44.4%; Pred. No. 31;
Matches 16; Conservative 1; Mismatches 15; Indels 4; Gaps 2;

QY 71 GTNIMHSHY--ANGALNGF--GLNAGYKKFQFQKS 102
DB 745 GINPEWISKVENLNALEFNKGNKNDPFSKVTQAKS 780

RESULT 11

US-08-487-032A-663
Sequence 663, Application US/08487032A
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 880
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,032A

US-08-487-032A-663
Sequence 663, Application US/08487032A
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 880
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,032A
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 663:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
US-08-487-032A-663

Query Match 5.8%; Score 46; DB 1; Length 214;
Best Local Similarity 46.2%; Pred. No. 8.5;
Matches 12; Conservative 2; Mismatches 6; Indels 6; Gaps 1;

QY 89 GINV-----GYKXKPFQKSLDNTSK 108
DB 129 GINVELQINPEVKDPTFKSISTNKK 154

RESULT 12
US-08-487-032A-671
Sequence 671, Application US/08487032A
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 880
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,032A

